IN THE SPECIFICATION:

Please replace the paragraph beginning at page 45, line 3, with the following rewritten paragraph:

The KCCs disclosed herein are thus homologous proteins, but when percentages are referred to herein, it is meant to refer to percent identity. The percent identities referenced herein were generated by alignments with the program GeneWorks (Oxford Molecular, Inc. of Campbell, California) and/or the BLAST program at NCBI (http://www.ncbi.nlm.nih.gov/BLAST/). Another commonly used alignment program is entitled CLUSTAL W and is described in Thompson et al. (1994) *Nucleic Acids Res* 22(22):4673-4680, among other places.

Please replace the paragraph beginning at page 107, line 22, with the following rewritten paragraph:

All cDNA clones were sequenced on both strands using fluorescent dye terminator chemistry (Applied Biosystems of Foster City, California). For cDNA sequence derived exclusively from PCR, at least two cDNAs from two separate PCR reactions were sequenced. Analyses of the nucleotide and amino acid sequences were performed using the GENEWORKS™ 2.5 and MACVECTOR™ 6.5 software packages (Oxford Molecular, Inc. of Campbell, California). Alignments and other analyses also made use of the computer programs BLAST (http://www.ncbi.nlm.nih.gov/blast), DNASTAR (DNASTAR, Inc. of Madison, Wisconsin), and SMART (simple modular architecture research tool) (Schultz et al. (1998) *Proc Natl Acad Sci USA* 95:5857-5864; Schultz et al. (2000) *Nuc Acids Res* 28:231-234; available from EMBL of Heidelberg, Germany).

Please replace the two (2) paragraphs beginning at page 111, line 16, with the following two (2) rewritten paragraphs:

The chromosomal localization of hKCC4 has been independently verified using the STS (sequence tag site) database. Thus the STS stSG1490 maps to chromosomal region 5p15, between the chromosome 5 markers D5S678 and D5S417. See the

UniSTS resource available from the NCBI website ~~Gene Map 99 URLs http://www.ncbi.nlm.nih.gov/genemap99/loc.cgi? ID=11342 and http://www.ncbi.nlm.nih.gov/genemap99/map.cgi? MAP=GB4&BIN=164&MARK= stSG1490~~.

The chromosomal localization of hKCC2 was also determined using the STS database. The STS WI-9597/stSG2530 is identical to nucleotides 5724-5896 of hKCC2. This STS maps to chromosomal region 20q13, between D20S836 and D20S888. See the UniSTS resource available from the NCBI website ~~Gene Map 99 URLs http://www.ncbi.nlm.nih.gov/ genemap99/ loc.cgi? ID=35899 and http://www.ncbi.nlm.nih.gov/genemap99/map.cgi? MAP=GB4&BIN=583&MARK= stSG2530~~.